

SU11_12				
014903				
CDS	BC013903	3173 bp	mRNA	linear
DEFINITION	Homo sapiens, Similar to <i>Homo</i> 2 (version 2)			PRJ_HG_SHP-2001
	IMAGE 2959199, mRNA, complete cds.			
SESSION	BC013903			
VERSION	BC013903.1	G1-15530242		
WORDS	MCA			
URC	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
MATERIAL	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
REFERENCE	I (bases 1 to 3173)			
AUTHORS	Stratford, R.			
TITLE	Direct Submission			
JOURNAL	Submitted (07-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Bethesda, MD 20892-2600, USA			

REMARK
COMMENT
NIH-MGC project URL: <http://mgc.nci.nih.gov>
Contact: MCC help desk
Email: carts@nci.nih.gov
Tissue procurement: ATC
cDNA library Preparation: Rubin Laboratory
cDNA library Arrayed by: The J.M.A.C.E. Consortium (JMC)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
contact: amadani@systemsbiology.org
Anup Madan, Rachael Ticknor, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kestelman and Anuradha Madan
clone distribution: MCC clone distribution information can be found

through the L.M.A.G.E. consortium/L.M.A. at: <http://image.lmni.gov>
 series: ITAL-plate: 2 grow; a column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mpNA 91-92, 57-54,
 location/qualifiers
 1..3173
 Source
 Organism: "Homo sapiens"
 RefSeq ID: 9666
 Alias: "MGI:1184 IMAGE:2459499"
 Feature: "Telomeric endogenous retrovirus"
 Chromosome: "11B-NH_MGC_15"

group. Further information can be found at
<http://www.sanger.ac.uk/IGP/chr6>
 RP11-507C10 is from the library RPC111.2 constructed by the group
<http://www.sanger.ac.uk/IGP/chr6> of Peter de Jong. For further details see
 VECTOR: PBACE3.6

This sequence is the entire insert of clone RP11-507C10. The true right end of clone RP11-14M11 is at 47323 in this sequence.

FEATURES

Location/Qualifiers

1..215705

/organism "Homo sapiens"

/db_xref "Taxon:4066"

/chromosome "6"

/map "q25;2-26"

/clone "RP11-507C10"

/clone_id "RPC11.2"

37002..37057

/note "Single clone region. Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."

156422..156454

/note "Sequence from uni-directional primer reads only."

156427..156427

50282..50282

c..c

49124..49124

q..q

59692..59692

t..t

ORIGIN

Alignment Scores:

Proj_Nr : 0_408

Score: 69.00

Percent_Similarity: 109.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 9

Gaps: 0

Length: 215705

Matches: 14

Conservative: 0

MisMatches: 0

Indels: 0

Gaps: 0

US-09-856-070-17 (1-14) x AI:589931 (1-215705)

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

ORIGIN

Alignment Scores:

Proj_Nr : AF450298

Score: 1446

Percent_Similarity: 100.00%

Best_Local_Similarity: 100.00%

Query_Match: 100.00%

DB: 134097

GAGAGAGAAAGAGCAGACATGCCAACAGGACCTT

134056

RESULT 14

OR

LHQIRQGNNTKQWIDEFAM"

misc_difference 1043
/note="q in clone TB4-2"

/replace="q"

misc_difference 1410
/note="q in clone TB4-2"

/replace="q"

misc_feature 1487
/replace="q"

/note="clone TB4-1"

BASE COUNT: 775 a 527 c 668 g 575 t

Alignment Scores:

Prod. No.:	0.0151	Length:	2545
Score:	66.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	92.86%	Mismatches:	0
Query Match:	95.65%	Deletions:	0
DR:	5	Gaps:	0

OS-09-856-070-17 (1-14) x AH014790 (1-2545)

YY 1 GluArgGluysGluGlnMetMetArgGluysGluGluLeu 14
 Db 1011 GAGAGGACACAGAGCAAAATTTTAAAGAAAAGAAGAATTC 1052

Search completed: January 16, 2003, 19:02:38
 Job time : 1248.6 secs